



## Sequence Listing

#6

## Sequence Listing

<110> Chen, Jian  
5 Filvaroff, Ellen  
Goddard, Audrey  
Gurney, Austin  
Li, Hanzhong  
Wood, William I.

10 <120> IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES  
THEREOF

<130> P1381-R1

15 <141> 1999-05-14

<150> US 60/085,579  
<151> 1998-05-15

20 <150> US 60/113,621  
<151> 1998-12-23

<160> 26

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<212> PRT  
<213> Homo sapiens

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1 5 10 15

35 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
35 40 45

40 Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
50 55 60

Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
45 65 70 75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
80 85 90

	Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
					95					100					105
5	Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
					110					115					120
	Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
					125					130					135
10	Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
					140					145					150
	Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
15					155					160					165
	Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
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 <211> 687  
 <212> DNA  
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 30 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 35 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300  
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 40 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
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 45 tgcccggcac cgcccgcac agggccttgc cgccagcgcg cagtcatgga 550  
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600

gccaggccag cagccccgaga ccatacctcct tgcacctttg tgccaagaaa 650

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<211> 197

<212> PRT

<213> Homo sapiens

10

<400> 3

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15

Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser
				20					25					30

His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly
				35					40					45

20

Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln
				50					55					60

25

Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His
				65					70					75

Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val
				80					85					90

30

Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser
				95					100					105

Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr
				110					115					120

35

Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile
				125					130					135

40

Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg
				140					145					150

Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg
				155					160					165

45

Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr
				170					175					180

Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg  
 185 190 195

Ser Val  
 197

5

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&lt;211&gt; 1047

&lt;212&gt; DNA

10 &lt;213&gt; Homo sapiens

&lt;400&gt; 4

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 gccaccatg acccctccct cagggggcac cccacagtc acggtacccc 150  
 acactgctac tcggctgagg aactgcccct cggccaggcc cccccacacc 200  
 20 tgctggctcg aggtgccaag tgggggcagg ctttgctgtg agccctgggtg 250  
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 tgctccagag cctgctgggtg ctgcgccgcc ggccctgctc ccgcgacggc 550  
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 cgtccccgct ggctgcacct gcgtgctgcc ccgttcagtg tgaccgccga 650  
 ggccgtgggg ccctagact ggacacgtgt gctccccaga gggcaccccc 700  
 40 tatttatgtg tatttattgt tatttatatg cctcccccaa cactaccctt 750  
 ggggtctggg cattccccgt gtctggagga cagcccccca ctgttctcct 800  
 45 catctccagc ctcagtagtt gggggtagaa ggagctcagc acctcttcca 850  
 gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt accttggtc 900

cctgtectgc tcccggcttc ccttacccta tcaactggcct caggccccgc 950  
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<212> DNA

10 <213> Homo sapiens

<220>

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<222> 105-115

15 <223> unknown base

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 gctcnnnnnn nnnnnaattc ggtacgaggc tggggttcag gcgggcagca 150  
 gctgcaggct gaccttgcag cttggcgga tggactggcc tcacaacctg 200  
 25 ctgtttcttc ttaccatttc catcttctg gggctgggccc agcccaggag 250  
 cccaaaagc aagaggaagg ggcaagggcg gcctgggccc ctggtcctctg 300  
 30 gccctacca ggtgccactg gacctggtgt cacggatgaa accgtatgcc 350  
 cgcattggagg agtatgagag gaacatcgag gagatgttgg ccagctgag 400  
 gaacagttca gagctggccc agagaaagtg tgagggtcaac ttgcagctgt 450  
 35 ggatgtccaa caagaggagc ctgtctcctt ggggctacag catcaaccac 500  
 gaccccagcc gtatccccgt ggacctccg aggcacggtg cctgtgtctg 550  
 40 ggcttgtgtg aacccttca ccatgcagga ggaccgcagc atggtgagcg 600  
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 cccgcacag ggccttgccg ccagcgcgca gtcattggaga ccatcgctgt 700  
 45 gggctgcacc tgcattcttct gaatcgacct ggcccagaag ccaggccagc 750  
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5 <211> 397

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<220>

10 <221> unknown

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20 agccaggagc cccaaaagca agaggaaggg gcaagggcgg cctgggcecn 150

tggcctggcc tcaccaggtg ccactggacc tgggtgtcacg gatgaaaccg 200

tatgcccgca tggaggagta tgagaggaac atcgaggaga tgggtggcca 250

25 gctgaggaac agctcanaag ctggcccaga gaaagtgtga ggtcaacttg 300

cagctgtgga tgtccaacaa gaaggagcct gtctcccttg gggctacaag 350

30 catcaaccac cgaccccagc cgtatccccg tgggaccttg ccgggac 397

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tccgtgcggc tgctccagag cctgctggtg ctgcgccgcc ggccttgctc 150

ccgcgacggc tcggggctcc ccacacctgg ggcctttgcc ttccacaccg 200

45

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&lt;213&gt; Artificial sequence

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&lt;211&gt; 24

&lt;212&gt; DNA

10 &lt;213&gt; Artificial sequence

&lt;400&gt; 9

gggacgtgga tgaactcggt gtgg 24

15 &lt;210&gt; 10

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

20 &lt;400&gt; 10

tatccacaga agctggcctt cgccgagtgc ctgtgcagag 40

&lt;210&gt; 11

&lt;211&gt; 155

25 &lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 11

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	1				5					10					15

	Ser	Leu	Glu	Ala	Ile	Val	Lys	Ala	Gly	Ile	Thr	Ile	Pro	Arg	Asn
					20					25					30

35	Pro	Gly	Cys	Pro	Asn	Ser	Glu	Asp	Lys	Asn	Phe	Pro	Arg	Thr	Val
					35					40					45

	Met	Val	Asn	Leu	Asn	Ile	His	Asn	Arg	Asn	Thr	Asn	Thr	Asn	Pro
					50					55					60

40	Lys	Arg	Ser	Ser	Asp	Tyr	Tyr	Asn	Arg	Ser	Thr	Ser	Pro	Trp	Asn
					65					70					75

	Leu	His	Arg	Asn	Glu	Asp	Pro	Glu	Arg	Tyr	Pro	Ser	Val	Ile	Trp
45					80					85					90

	Glu	Ala	Lys	Cys	Arg	His	Leu	Gly	Cys	Ile	Asn	Ala	Asp	Gly	Asn
					95					100					105

	Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu	
	110	115 120
5	Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu	
	125	130 135
	Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile	
	140	145 150
10	Val His His Val Ala	
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15	<211> 408	
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	20	25 30
	Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val	
30	35	40 45
	Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu	
	50	55 60
35	Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn	
	65	70 75
	Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu	
	80	85 90
40	Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile	
	95	100 105
	Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg	
45	110	115 120
	Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp	
	125	130 135



	Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg	140	145	150
5	Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln	155	160	165
	Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe	170	175	180
10	Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu	185	190	195
	Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	200	205	210
15	Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	215	220	225
	Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	230	235	240
	Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu	245	250	255
25	Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	260	265	270
	His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser	275	280	285
30	Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	290	295	300
	Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser	305	310	315
	Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val	320	325	330
40	Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn	335	340	345
	Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	350	355	360
45	Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys	365	370	375

	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	
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5	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
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	Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser	
					20					25					30	
25	His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly	
					35					40					45	
	Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln	
30					50					55					60	
	Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His	
					65					70					75	
35	Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val	
					80					85					90	
	Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser	
					95					100					105	
40	Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr	
					110					115					120	
	Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile	
45					125					130					135	
	Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg	
					140					145					150	

	Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg	
					155					160					165	
5	Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr	
					170					175					180	
	Glu	Phe	Ile	His	Val	Pro	Val	Gly	Cys	Thr	Cys	Val	Leu	Pro	Arg	
					185					190					195	
10	Ser	Val	Pro	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
					200					205					210	
	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	
15					215					220					225	
	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
					230					235					240	
20	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
					245					250					255	
	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	
					260					265					270	
25	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
					275					280					285	
	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	
30					290					295					300	
	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
					305					310					315	
35	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	
					320					325					330	
	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	
					335					340					345	
40	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
					350					355					360	
	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	
45					365					370					375	
	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
					380					385					390	

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 395 400 405

5 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 410 415 420

Leu Ser Pro Gly Lys  
 425

10 <210> 14  
 <211> 212  
 <212> PRT  
 <213> Homo sapiens

15 <400> 14  
 Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser  
 1 5 10 15

20 Leu Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val  
 20 25 30

Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln  
 35 40 45

25 Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile  
 50 55 60

30 Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser  
 65 70 75

Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu  
 80 85 90

35 Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly  
 95 100 105

Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu  
 110 115 120

40 Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser  
 125 130 135

45 Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu  
 140 145 150

Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr  
 155 160 165

	Thr	Pro	Asp	Pro	Thr	Thr	Asn	Ala	Ser	Leu	Leu	Thr	Lys	Leu	Gln	
					170					175					180	
5	Ala	Gln	Asn	Gln	Trp	Leu	Gln	Asp	Met	Thr	Thr	His	Leu	Ile	Leu	
					185					190					195	
	Arg	Ser	Phe	Lys	Glu	Phe	Leu	Gln	Ser	Ser	Leu	Arg	Ala	Leu	Arg	
					200					205					210	
10	Gln	Met														
		212														
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					20					25					30	
25	Ala	Ser	Leu	Arg	Leu	Leu	Asp	His	Arg	Ala	Leu	Val	Cys	Ser	Gln	
					35					40					45	
	Pro	Gly	Leu	Asn	Cys	Thr	Val	Lys	Asn	Ser	Thr	Cys	Leu	Asp	Asp	
30					50					55					60	
	Ser	Trp	Ile	His	Pro	Arg	Asn	Leu	Thr	Pro	Ser	Ser	Pro	Lys	Asp	
					65					70					75	
35	Leu	Gln	Ile	Gln	Leu	His	Phe	Ala	His	Thr	Gln	Gln	Gly	Asp	Leu	
					80					85					90	
	Phe	Pro	Val	Ala	His	Ile	Glu	Trp	Thr	Leu	Gln	Thr	Asp	Ala	Ser	
					95					100					105	
40	Ile	Leu	Tyr	Leu	Glu	Gly	Ala	Glu	Leu	Ser	Val	Leu	Gln	Leu	Asn	
					110					115					120	
	Thr	Asn	Glu	Arg	Leu	Cys	Val	Arg	Phe	Glu	Phe	Leu	Ser	Lys	Leu	
45					125					130					135	
	Arg	His	His	His	Arg	Arg	Trp	Arg	Phe	Thr	Phe	Ser	His	Phe	Val	
					140					145					150	

	Val	Asp	Pro	Asp	Gln	Glu	Tyr	Glu	Val	Thr	Val	His	His	Leu	Pro
					155					160					165
5	Lys	Pro	Ile	Pro	Asp	Gly	Asp	Pro	Asn	His	Gln	Ser	Lys	Asn	Phe
					170					175					180
	Leu	Val	Pro	Asp	Cys	Glu	His	Ala	Arg	Met	Lys	Val	Thr	Thr	Pro
					185					190					195
10	Cys	Met	Ser	Ser	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Val	Glu
					200					205					210
	Thr	Leu	Glu	Ala	His	Gln	Leu	Arg	Val	Ser	Phe	Thr	Leu	Trp	Asn
15					215					220					225
	Glu	Ser	Thr	His	Tyr	Gln	Ile	Leu	Leu	Thr	Ser	Phe	Pro	His	Met
					230					235					240
20	Glu	Asn	His	Ser	Cys	Phe	Glu	His	Met	His	His	Ile	Pro	Ala	Pro
					245					250					255
	Arg	Pro	Glu	Glu	Phe	His	Gln	Arg	Ser	Asn	Val	Thr	Leu	Thr	Leu
					260					265					270
25	Arg	Asn	Leu	Lys	Gly	Cys	Cys	Arg	His	Gln	Val	Gln	Ile	Gln	Pro
					275					280					285
	Phe	Phe	Ser	Ser	Cys	Leu	Asn	Asp	Cys	Leu	Arg	His	Ser	Ala	Thr
30					290					295					300
	Val	Ser	Cys	Pro	Glu	Met	Pro	Asp	Thr	Pro	Glu	Pro	Ile	Pro	Asp
					305					310					315
35	Tyr	Met	Pro	Leu	Trp										
					320										

&lt;210&gt; 16

&lt;211&gt; 543

40 &lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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45

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ggcctgggccc cctggcccct ggcctcacc aggtgccact ggacctggtg 150

tcacggatga aaccgtatgc ccgcatggag gagtatgaga ggaacatcga 200  
 ggagatggtg gccagctga ggaacagctc agagctggcc cagagaaagt 250  
 5 gtgagggtcaa cttgcagctg tggatgtcca acaagaggag cctgtctccc 300  
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 10 ggaggcacgg tgcctgtgtc tgggctgtgt gaaccccttc accatgcagg 400  
 aggaccgcag catggtgagc gtgccggtgt tcagccaggt tcctgtgcgc 450  
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<210> 17

<211> 594

20 <212> DNA

<213> Homo sapiens

<400> 17

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 cacactgcta ctcggtgag gaactgcccc tcggccaggc cccccacac 150  
 30 ctgctggctc gaggtgcaa gtggggggcag gctttgctg tagccctggt 200  
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 ctacgaccca gtgcccggtg ctgcggccgg aggaggtgtt ggaggcagac 300  
 35 acccaccagc gctccatctc acctggaga tacctgttgg acacggatga 350  
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 40 gtatcgatgc acggacgggc cgcgagacag ctgcgctcaa ctccgtgcgg 450  
 ctgctccaga gcctgctggt gctgcgccgc cggccctgct cccgcgacgg 500  
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5 <220>  
 <223> Artificial sequence 1-9

<400> 18  
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<210> 19  
 <211> 157  
 <212> PRT

15 <213> Homo sapiens

<400> 19  
 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His  
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20 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn  
 20 25 30

25 Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp  
 35 40 45

Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser  
 50 55 60

30 Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu  
 65 70 75

Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys  
 80 85 90

35 Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr  
 95 100 105

40 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu  
 110 115 120

Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu  
 125 130 135

45 Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val  
 140 145 150

Tyr Phe Gly Ile Ile Ala Leu



17

	Leu	Gln	Ile	Gln	Leu	His	Phe	Ala	His	Thr	Gln	Gln	Gly	Asp	Leu	
					80					85					90	
5	Phe	Pro	Val	Ala	His	Ile	Glu	Trp	Thr	Leu	Gln	Thr	Asp	Ala	Ser	
					95					100					105	
	Ile	Leu	Tyr	Leu	Glu	Gly	Ala	Glu	Leu	Ser	Val	Leu	Gln	Leu	Asn	
					110					115					120	
10	Thr	Asn	Glu	Arg	Leu	Cys	Val	Arg	Phe	Glu	Phe	Leu	Ser	Lys	Leu	
					125					130					135	
	Arg	His	His	His	Arg	Arg	Trp	Arg	Phe	Thr	Phe	Ser	His	Phe	Val	
					140					145					150	
15	Val	Asp	Pro	Asp	Gln	Glu	Tyr	Glu	Val	Thr	Val	His	His	Leu	Pro	
					155					160					165	
	Lys	Pro	Ile	Pro	Asp	Gly	Asp	Pro	Asn	His	Gln	Ser	Lys	Asn	Phe	
20					170					175					180	
	Leu	Val	Pro	Asp	Cys	Glu	His	Ala	Arg	Met	Lys	Val	Thr	Thr	Pro	
					185					190					195	
25	Cys	Met	Ser	Ser	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Val	Glu	
					200					205					210	
	Thr	Leu	Glu	Ala	His	Gln	Leu	Arg	Val	Ser	Phe	Thr	Leu	Trp	Asn	
					215					220					225	
30	Glu	Ser	Thr	His	Tyr	Gln	Ile	Leu	Leu	Thr	Ser	Phe	Pro	His	Met	
					230					235					240	
	Glu	Asn	His	Ser	Cys	Phe	Glu	His	Met	His	His	Ile	Pro	Ala	Pro	
35					245					250					255	
	Arg	Pro	Glu	Glu	Phe	His	Gln	Arg	Ser	Asn	Val	Thr	Leu	Thr	Leu	
					260					265					270	
40	Arg	Asn	Leu	Lys	Gly	Cys	Cys	Arg	His	Gln	Val	Gln	Ile	Gln	Pro	
					275					280					285	
	Phe	Phe	Ser	Ser	Cys	Leu	Asn	Asp	Cys	Leu	Arg	His	Ser	Ala	Thr	
					290					295					300	
45	Val	Ser	Cys	Pro	Glu	Met	Pro	Asp	Thr	Pro	Glu	Pro	Ile	Pro	Asp	
					305					310					315	

Tyr Met Pro Leu Trp His His His His His His His His  
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<210> 23

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<212> PRT

<213> Artificial

**<220>**

10 <223> Artificial sequence 1-175

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Ile Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg  
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Lys Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln  
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20

Val	Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met
				35					40					45

Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg  
50 55 60

25

Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln  
65 70 75

Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser  
80 85 90

30

Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala  
95 100 105

35

Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu  
110 115 120

Asp	Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val
				125					130					135

40

Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg  
140 145 150

Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile  
155 160 165

45

Phe Gly His His His His His His His His  
170 175

<210> 24  
 <211> 206  
 <212> PRT  
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<220>  
 <223> Artificial sequence 1-206

<400> 24

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	1				5					10					15
	Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser
					20					25					30
15	His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly
					35					40					45
	Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln
20					50					55					60
	Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His
					65					70					75
25	Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val
					80					85					90
	Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser
					95					100					105
30	Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr
					110					115					120
	Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile
35					125					130					135
	Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg
					140					145					150
40	Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg
					155					160					165
	Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr
					170					175					180
45	Glu	Phe	Ile	His	Val	Pro	Val	Gly	Cys	Thr	Cys	Val	Leu	Pro	Arg
					185					190					195

Ser Val Gly His His His His His His His His  
200 205 206

<210> 25

5 <211> 271

<212> PRT

<213> Homo sapiens

<400> 25

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10      Met Ala Lys Val  Pro  Asp Met  Phe  Glu  Asp  Leu  Lys  Asn  Cys  Tyr
          1              5              10              15

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Ser Glu Asn Glu Glu Asp Ser Ser Ser Ile Asp His Leu Ser Leu  
20 25 30

15 Asn Gln Lys Ser Phe Tyr His Val Ser Tyr Gly Pro Leu His Glu  
35 40 45

20 Gly Cys Met Asp Gln Ser Val Ser Leu Ser Ile Ser Glu Thr Ser 60  
50 55

Lys Thr Ser Lys Leu Thr Phe Lys Glu Ser Met Val Val Val Ala  
65 70 75

25    Thr Asn Gly Lys Val Leu Lys Lys Arg Arg Leu Ser Leu Ser Gln  
                        80                        85                        90

Ser Ile Thr Asp Asp Asp Leu Glu Ala Ile Ala Asn Asp Ser Glu  
95 100 105

30  
Glu Glu Ile Ile Lys Pro Arg Ser Ala Pro Phe Ser Phe Leu Ser  
110 115 120

Asn Val Lys Tyr Asn Phe Met Arg Ile Ile Lys Tyr Glu Phe Ile  
35                   125                   130                   135

Leu Asn Asp Ala Leu Asn Gln Ser Ile Ile Arg Ala Asn Asp Gln  
140 145 150

40 Tyr Leu Thr Ala Ala Ala Leu His Asn Leu Asp Glu Ala Val Lys  
155 160 165

Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp Asp Ala Lys Ile  
170 175 180

45 Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr Val Thr Ala  
185 190 195

	Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro Glu Ile	200	205	210
5	Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe Trp	215	220	225
	Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro	230	235	240
10	Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala	245	250	255
	Gly Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln	260	265	270
15	Ala			
	271			
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20	<211> 177			
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	<400> 26			
25	Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu	1	5	10
				15
	Leu Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg	20	25	30
30	Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln	35	40	45
	Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu	50	55	60
35				
	Gln Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro	65	70	75
40	Ile Glu Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met	80	85	90
	Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu	95	100	105
45	Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp	110	115	120

	Lys	Arg	Phe	Ala	Phe	Ile	Arg	Ser	Asp	Ser	Gly	Pro	Thr	Thr	Ser
					125					130					135
5	Phe	Glu	Ser	Ala	Ala	Cys	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Ala	Met
					140					145					150
	Glu	Ala	Asp	Gln	Pro	Val	Ser	Leu	Thr	Asn	Met	Pro	Asp	Glu	Gly
					155					160					165
10	Val	Met	Val	Thr	Leu	Phe	Tyr	Phe	Gln	Glu	Asp	Glu			
					170					175		177			